

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd

5

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

10

<140>

<141>

<160> 27

15

<170> PatentIn Ver. 2.1

<210> 1

<211> 325

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<212> PRT

<213> Penicillium citrinum

<400> 1

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20 25 30

30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

35

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

40

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 5 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 10 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 15 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 20 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 25 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 30 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 35 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
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Lys Asn Leu Ser Ala
325

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<212> DNA
<213> Penicillium citrinum

10 <220>
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<222> (1).. (978)

<400> 2

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| | Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro | |
| | 1 5 10 15 | |
| 20 | ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc | 96 |
| | Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr | |
| | 20 25 30 | |
| 25 | tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac | 144 |
| | Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp | |
| | 35 40 45 | |
| 30 | tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt | 192 |
| | Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg | |
| | 50 55 60 | |
| 35 | gac ttc ctg aag gag aac ccc tog gtg aag cgt gag gac atc ttc gtc | 240 |
| | Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val | |
| | 65 70 75 80 | |
| 40 | tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg | 288 |
| | Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp | |
| | 85 90 95 | |
| 40 | tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg | 336 |
| | Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met | |
| | 100 105 110 | |

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 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125

5 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

10 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

15 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt 528
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175

20 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190

25 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc 624
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205

30 tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tgc cag aac 672
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220

35 cag gtt ccc acc acc ggt gag ogg gtc agc gag aac aag act ctg aac 720
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240

40 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255

tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp

| | 275 | 280 | 285 | |
|----|---|-----|-----|-----|
| | t t t g a a g c c a t c a a t g c c g t t g c c a a g g g t c g t c a c t t c c g t t t c g t c | | | 912 |
| | Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val | | | |
| 5 | 290 | 295 | 300 | |
| | a a c a t g a a g g a t a c t t t c g g a t a t g a t g t c t g g c c c g a g g a g a c c g c c | | | 960 |
| | Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala | | | |
| | 305 | 310 | 315 | 320 |
| 10 | | | | 978 |
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| | <400> 4 | | | |
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| 40 | | | | |
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| | <212> PRT | | | |
| | <213> Penicillium citrinum | | | |

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1 5 10 15

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Lys

10 <210> 6
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<213> *Penicillium citrinum*

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1 5 10

20 <210> 7
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<211> 20
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35 <220>
<223> Description of Artificial Sequence: Designed
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10

<210> 13

<211> 20

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<210> 15

<211> 697

<212> DNA

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<213> Escherichia coli

<400> 15


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agtgaagggtt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccggttac 180
cgtoncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnccgt 240
5 gaattcctga aggaaaaacc ctcggtgaag cgtgaggaca tcttgcctg caccaagggtg 300
tggaaccaac tccaccgtta tgaggacgtc ctctggtcca ttgacnaac cctgaagcgt 360
cttggacttg actacgttga tatgttcctc gttcactggc ccattgctgc cgaaaaaat 420
ggccagggtg agcccaaaat tggccctgac ggcaaatc tcttctcaa ggacctgacc 480
gaaanccna nccacctgg cgogctatgg aaaaaattt tgangatccc aaggccaggt 540
10 ccattggtgt ttccaattgg accattgcg accttgagaa gatgtccaag ttngccaagg 600
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30 <210> 17
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35 <220>
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40 <210> 18
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<212> DNA

<213> Escherichia coli

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5  cgctotaaaa ctantggatc ccccgggctg caggaattcg gcgccgcggg atccttcato 60
   cccatcatgt otaacggaaa gactttcaca ttgagcaacg gcgtcaagat tcctggcgto 120
   ggctttggta ccttcgctag tgaaggttcc aaggcgagaga cctatactgc tgtcaccact 180
   gccotgaaga ccggttaccg tcaattggac tgtgcctggg actacctgaa cgagggtgag 240
   gttggtgagg gtatccgtga cticctgaag gagaaccctt oggtgaagcg tgaggacato 300
10  ttctgtctgca ccaagggtgt gaaccacotc c                                     331

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<210> 19

<211> 743

15 <212> DNA

<213> Escherichia coli

<400> 19

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   caagaacatt atgcccgtgg cctactctcc totgggctcg cagaaccagg ttcccaccac 120
   cgggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac 180
   ccttgctcag gttottattg cctgggggtot gcgccgtggc tacgtcgttc tccccaagag 240
   ctccaacccc aagcgcatcg agtccaactt caagagcatt gagctctcog atgccgactt 300
   tgaagccatc aatgocgttg ccaagggtog tcaattccgt ttogtcaaca tgaaggatac 360
25  tttoggatat gatgtctggc ccgaggagac cgccaagaac ctgtctgcgt gaatctctac 420
   gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatncc aaanttttg 480
   agggtttctt ggttgaaaac gtttantgan ccgaantga angaatagat gancntgatt 540
   tctccaaaaa aaaaaaaaaa aaaaaaggtc cggcgccgct ccnngggggg gcccggttcc 600
   caattcnccc cttatnattg aattcttttt taanggggnc aaattooncc nnatttcoct 660
30  cnanattggn nggcccctc caaactttcn tcntnaaagg gncccaatto ccccccatt 720
   aantggantt cctntttacc ttt                                     743

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40 <223> Description of Artificial Sequence: Designed
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21

<210> 27
 <211> 786
 <212> DNA
 <213> Escherichia coli

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 <222> (1).. (786)

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15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30

20

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt 144
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
 35 40 45

25

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60

30

gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att 240
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80

35

aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95

40

aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110

att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att 384
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

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<210> 22

<211> 417

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<213> Escherichia coli

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agaagaatgg ccaggggtgag cccaagattg gccctgacgg caaatacgtc attctcaagg 180
acctgaccga gaaccccgag cccacatggc gcgctatgga gaagatttat gaggatcgca 240
aggccaggto cattggtgtc tccaactgga ccattgocga ccttgagaag atgtccaagt 300
tcgccaaggt catgcctcac gcccaaccaga tcgagattca ccccttcoctg cccaacgagg 360
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<213> Artificial Sequence

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| | Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser | |
| | 130 135 140 | |
| 5 | agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca | 480 |
| | Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala | |
| | 145 150 155 160 | |
| 10 | agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac | 528 |
| | Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr | |
| | 165 170 175 | |
| 15 | gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat | 576 |
| | Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn | |
| | 180 185 190 | |
| 20 | aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat | 624 |
| | Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp | |
| | 195 200 205 | |
| 25 | gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att | 672 |
| | Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile | |
| | 210 215 220 | |
| 30 | ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc | 768 |
| | Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe | |
| | 245 250 255 | |
| 35 | caa gca gga ogc gga taa | 786 |
| | Gln Ala Gly Arg Gly | |
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<222> (1).. (978)

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| Met | Ser | Asn | Gly | Lys | Thr | Phe | Thr | Leu | Ser | Asn | Gly | Val | Lys | Ile | Pro | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ggc | gtc | ggc | ttt | ggc | acc | ttc | gct | agt | gaa | ggc | tcc | aag | ggc | gag | acc | 96 |
| Gly | Val | Gly | Phe | Gly | Thr | Phe | Ala | Ser | Glu | Gly | Ser | Lys | Gly | Glu | Thr | |
| | | 20 | | | | | 25 | | | | | 30 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | act | gct | gtc | acc | act | gcc | ctg | aag | acc | ggc | tac | cgt | cac | ttg | gac | 144 |
| Tyr | Thr | Ala | Val | Thr | Thr | Ala | Leu | Lys | Thr | Gly | Tyr | Arg | His | Leu | Asp | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgt | gcc | tgg | tac | tac | ctg | aac | gag | ggc | gag | gtt | ggc | gag | ggc | atc | cgt | 192 |
| Cys | Ala | Trp | Tyr | Tyr | Leu | Asn | Glu | Gly | Glu | Val | Gly | Glu | Gly | Ile | Arg | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gac | ttc | ctg | aag | gag | aac | ccc | tgc | gtg | aag | cgt | gag | gac | atc | ttc | gtc | 240 |
| Asp | Phe | Leu | Lys | Glu | Asn | Pro | Ser | Val | Lys | Arg | Glu | Asp | Ile | Phe | Val | |
| 65 | | | | 70 | | | | 75 | | | | | 80 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgc | acc | aag | gtg | tgg | aac | cac | ctc | cac | cgt | tat | gag | gac | gtc | ctc | tgg | 288 |
| Cys | Thr | Lys | Val | Trp | Asn | His | Leu | His | Arg | Tyr | Glu | Asp | Val | Leu | Trp | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tcc | att | gac | gac | tcc | ctg | aag | cgt | ctt | gga | ctt | gac | tac | gtt | gat | atg | 336 |
| Ser | Ile | Asp | Asp | Ser | Leu | Lys | Arg | Leu | Gly | Leu | Asp | Tyr | Val | Asp | Met | |
| | | 100 | | | | | 105 | | | | | 110 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | ctc | gtt | cac | tgg | ccc | att | gct | gcc | gag | aag | aat | ggc | cag | ggc | gag | 384 |
| Phe | Leu | Val | His | Trp | Pro | Ile | Ala | Ala | Glu | Lys | Asn | Gly | Gln | Gly | Glu | |
| | 115 | | | | 120 | | | | | | 125 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccc | aag | att | ggc | cct | gac | ggc | aaa | tac | gtc | att | ctc | aag | gac | ctg | acc | 432 |
| Pro | Lys | Ile | Gly | Pro | Asp | Gly | Lys | Tyr | Val | Ile | Leu | Lys | Asp | Leu | Thr | |
| 40 | 130 | | | | 135 | | | | 140 | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | aac | ccc | gag | ccc | aca | tgg | cgc | gct | atg | gag | aag | att | tat | gag | gat | 480 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

aag aac ctg tct gog tga atctctaoga aattataa

996

Lys Asn Leu Ser Ala

325

5

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR

15

<400> 29

cggtatccgtt cacgcagaca gggtcttgg

29

<210> 30

<211> 978

20

<212> DNA

<213> Penicillium citrinum

<220>

<221> CDS

25

<222> (1).. (978)

<400> 30

atg tct aac gga aag act ttc aca ttg ago aac ggc gtc aag att oct 48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro

30

1

5

10

15

ggc gtc ggc ttt ggt acc ttc got agt gaa ggt tcc aag ggc gag acc 96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

35

tat act got gtc acc act gcc ctg aag acc ggt tac ogt cac ttg gac 144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

40

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

5 gag ttc ctg aag gag aac ccc tgc gtg aag cgt gag gac atc ttc gtc 240
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

10 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

15 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

20 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag 384
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125

25 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

30 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

35 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ott 528
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175

40 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190

45 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc 624
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205

50 tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tgc cag aac 672
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220

55 cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac 720

Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225 230 235 240

5 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
245 250 255

10 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
260 265 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
275 280 285

15 ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
290 295 300

20 aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
305 310 315 320

25 aag aac ctg tot gcg tga 978
Lys Asn Leu Ser Ala
325

<210> 31

<211> 27

30 <212> DNA

<213> Artificial Sequence

<220>

35 <223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

<400> 31

gccatggcta tgtataaaga tttagaa 27

40

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

<400> 32

cggatcggtt atccgggtcc tgc

23

10

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

20

<400> 33

cggatccgag cgccaatac gcaaaccg

28

<210> 34

<211> 385

25

<212> PRT

<213> Corynebacterium sp.

<400> 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr

30

1

5

10

15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val

20

25

30

35

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro

35

40

45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly

50

55

60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

5 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

10 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
15 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145 150 155 160

20 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180 185 190

25 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
30 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
260 265 270

40 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
290 295 300

5 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
325 330 335

10

Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
340 345 350

15

Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
355 360 365

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

20

Arg
385

<210> 35

25

<211> 1158

<212> DNA

<213> Corynebacterium sp.

<220>

30

<221> CDS

<222> (1).. (1158)

<400> 35

35

atg aag gcg atc cag tac acg oga atc ggc ggc gaa ooc gaa ctc acg 48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

40

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

acc gct gct ggc gtc tgc cac tgc gac gac ttc atc atg agc ctg ccc 144

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
 35 40 45

5 gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc 192
 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
 50 55 60

10 gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc 240
 Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

15 gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg 288
 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
 85 90 95

20 cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc 336
 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 100 105 110

25 gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc 384
 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

30 atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac 432
 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

35 ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac 480
 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

40 gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt 528
 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

576 gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc
 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

624 cac ctc tog gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag
 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

| | | |
|----|---|------|
| | ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac | 672 |
| | Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp | |
| | 210 215 220 | |
| 5 | aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc | 720 |
| | Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala | |
| | 225 230 235 240 | |
| 10 | gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg | 768 |
| | Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala | |
| | 245 250 255 | |
| 15 | atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg | 816 |
| | Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly | |
| | 260 265 270 | |
| 20 | gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag | 864 |
| | Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu | |
| | 275 280 285 | |
| 25 | gct tog gtg aca gtt cag tat tgg ggt gcc cgc aac gag ttg atc gaa | 912 |
| | Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu | |
| | 290 295 300 | |
| 30 | ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac | 960 |
| | Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp | |
| | 305 310 315 320 | |
| 35 | ctt cag tct cga caa cgg tgc cga agc gta tgc acg act ggc tgc cgg | 1008 |
| | Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg | |
| | 325 330 335 | |
| 40 | aac gct cag cgg cag tgc ggt tgt ggt ccc tgg tct gta gta ccg aca | 1056 |
| | Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr | |
| | 340 345 350 | |
| 45 | gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tgc att | 1104 |
| | Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile | |
| | 355 360 365 | |
| 50 | cgg ccg ggc atc agt gtc aga aat tgc gtg tgc gct agc tgc acg cct | 1152 |

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

5 cga tga
Arg
385

1158